



BOX SEQUENCE

Applicants: C.L. Steele et al.

Attorney Docket No.: WSUR118414

Application No.: 10/025,145

Group Art Unit: 1638

Filed: December 19, 2001

Title: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

RESPONSE TO THE NOTICE TO COMPLY WITH REQUIREMENTS FOR
PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE
AND/OR AMINO ACID SEQUENCE DISCLOSURE

Seattle, Washington 98101
June 27, 2002

TO THE COMMISSIONER FOR PATENTS:

Please enter the substitute sequence listing into the above-referenced patent application. Applicants note that SEQ ID NO:11 was erroneously identified as an artificial sequence in the original sequence listing. As set forth at page 31, lines 1-17, SEQ ID NO:11 discloses the sequence of a Grand Fir cDNA molecule. Thus, SEQ ID NO:11 is not an artificial sequence, and is not referred to as such in the substitute sequence listing.

Respectfully submitted,

CHRISTENSEN O'CONNOR
JOHNSON KINDNESS^{PLLC}

Barry F. McGurl
Registration No. 43,340
Direct Dial No. 206.695.1775

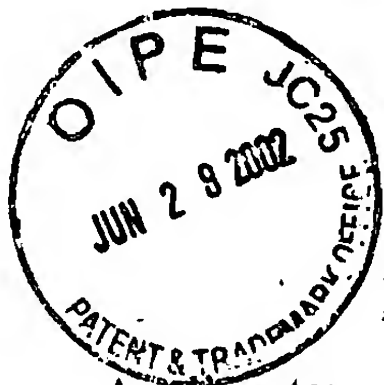
I hereby certify that this correspondence is being transmitted via FEDERAL EXPRESS addressed to the U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2001 South Clark Place, Arlington, VA 22202, on the below date.

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LAW OFFICES OF
CHRISTENSEN O'CONNOR JOHNSON KINDNESS^{PLLC}
1420 Fifth Avenue
Suite 2800
Seattle, Washington 98101
206.682.8100



T.D. O.B.I.C.O. / B.A. / S.E.
BOX SEQUENCE

#3

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: C.L. Steele et al.

Attorney Docket No.: WSUR118414

Application No.: 10/025,145

Group Art Unit: 1638

Filed: December 19, 2001

Title: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

TRANSMITTAL OF SUBSTITUTE SEQUENCE LISTING

Seattle, Washington 98101

June 27, 2002

TO THE COMMISSIONER FOR PATENTS:

A. Substitute Sequence Listing:

Transmitted herewith is a Response to the outstanding Formalities Letter, including the following:

1. Substitute sequence listing in computer readable form (diskette) and in paper copy form (83 pages), for entry into the above-identified application. The contents of the computer readable copy and paper copy of the substitute sequence listing are the same and contain no new matter.
2. Copy of the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosure
3. Copy of the Raw Sequence Listing Error Report.

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CHRISTENSEN O'CONNOR JOHNSON KINDNESS^{PLLC}
1420 Fifth Avenue
Suite 2800
Seattle, Washington 98101
206.682.8100



B. Additional Fee Charges or Credit for Overpayment

The Commissioner is hereby authorized to charge any fees under 37 C.F.R. §§ 1.16, 1.17 and 1.18 which may be required during the entire pendency of the application, or credit any overpayment, to Deposit Account No. 03-1740. This authorization also hereby includes a request for any extensions of time of the appropriate length required upon the filing of any reply during the entire prosecution of this application. A copy of this document is enclosed.

Respectfully submitted,

CHRISTENSEN O'CONNOR
JOHNSON KINDNESS^{PLLC}

Barry F. McGurl
Registration No. 43,340
Direct Dial No. 206.695.1775

I hereby certify that this correspondence is being transmitted via FEDERAL EXPRESS addressed to the U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2001 South Clark Place, Arlington, VA 22202, on the below date.

Date:

6/27/02

BFM:jlj

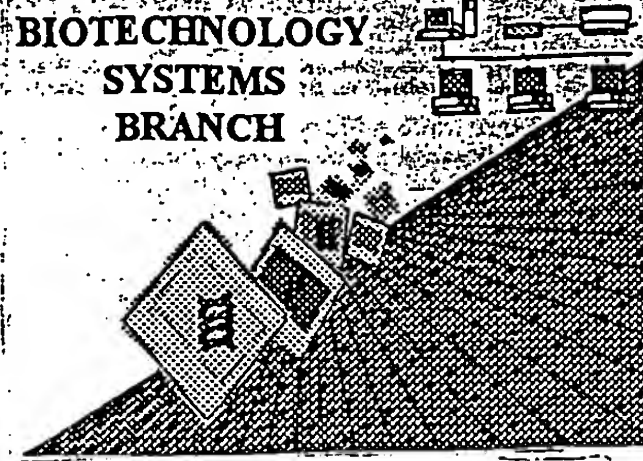
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1420 Fifth Avenue
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Seattle, Washington 98101
206.682.8100



0590

0450

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/025,145
Source: OIPE
Date Processed by STIC: 1/15/2002

Anjum,
I couldn't find disk

Anne.

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission

User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

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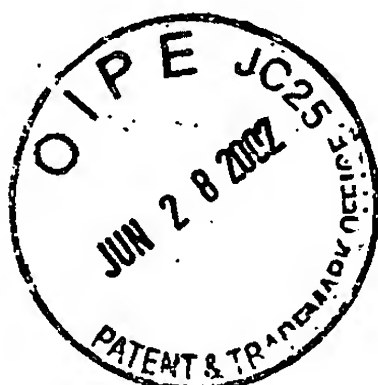
SUGGESTED CORRECTION

SERIAL NUMBER: 10/025,145

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) 11 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/025,145

DATE: 01/15/2002
TIME: 18:55:54

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Output Set: N:\CRF3\01152002\J025145.raw

Does Not Comply
Corrected Diskette Needed

6-7

OK

3 <110> APPLICANT: Croteau, Rodney B
4 Bohlmann, Joerg
5 Steele, Christopher L
6 Phillips, Michael A
8 <120> TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
10 <130> FILE REFERENCE: WSUR18414
12 <140> CURRENT APPLICATION NUMBER: US/10/025,145
13 <141> CURRENT FILING DATE: 2001-12-19
15 <150> PRIOR APPLICATION NUMBER: 09/360,545
16 <151> PRIOR FILING DATE: 1999-07-26
18 <150> PRIOR APPLICATION NUMBER: 60/052,249
19 <151> PRIOR FILING DATE: 1997-07-11
21 <150> PRIOR APPLICATION NUMBER: PCT/US98/14528
22 <151> PRIOR FILING DATE: 1998-07-10
24 <160> NUMBER OF SEQ ID NOS: 107
26 <170> SOFTWARE: PatentIn Ver. 2.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 2196
30 <212> TYPE: DNA
31 <213> ORGANISM: Abies grandis
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (69)..(1952)
36 <223> OTHER INFORMATION: Clone AG2.2 encoding myrcene synthase
38 <400> SEQUENCE: 1
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42 Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys
43 1 5 10
45 ctg cgc aag tcg ttg atc agt tca att cat gaa cat aag cct ccc tat 158
46 Leu Arg Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr
47 15 20 25 30
49 aga aca atc cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg 206
50 Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr
51 35 40 45
53 cct tcc atg agc atc agt ttg gcc acc gct gca cct gat gat ggt gta 254
54 Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val
55 50 55 60
57 caa aga cgc ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc 302
58 Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe
59 65 70 75
61 ata cag tct cta tca acg cct tat ggg gaa ccc tct tac cag gaa cgt 350
62 Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg
63 80 85 90
65 gct gag aga tta att gtg gag gta aag aag ata ttc aat tca atg tac 398
66 Ala Glu Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr
67 95 100 105 110

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/025,145

DATE: 01/15/2002

TIME: 18:55:54

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71 115 120 125
73 ctt tgg ata gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc 494
74 Leu Trp Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe
75 130 135 140
77 aag aac gag ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag 542
78 Lys Asn Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu
79 145 150 155
81 gaa aac ggc att gga tgt ggg aga gac agt att gtt act gat ctc aac 590
82 Glu Asn Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn
83 160 165 170
85 tca act gcg ttg ggg ttt cga act ctt cga tta cac ggg tac act gta 638
86 Ser Thr Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val
87 175 180 185 190
89 tct cca gag gtt tta aaa gct ttt caa gat caa aat gga cag ttt gta 686
90 Ser Pro Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val
91 195 200 205
93 tgc tcc ccc ggt cag aca gag ggt gag atc aga agc gtt ctt aac tta 734
94 Cys Ser Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu
95 210 215 220
97 tat cgg gct tcc ctc att gcc ttc cct ggt gag aaa gtt atg gaa gaa 782
98 Tyr Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu
99 225 230- 235
101 gct gaa atc ttc tcc aca aga tat ttg aaa gaa gct cta caa aag att 830
102 Ala Glu Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile
103 240 245 250
105 cca gtc tcc gct ctt tca caa gag ata aag ttt gtt atg gaa tat ggc 878
106 Pro Val Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly
107 255 260 265 270
109 tgg cac aca aat ttg cca aga ttg gaa gca aga aat tac ata gac aca 926
110 Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr
111 275 280 285
113 ctt gag aaa gac acc agt gca tgg ctc aat aaa aat gct ggg aag aag 974
114 Leu Glu Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys
115 290 295 300
117 ctt tta gaa ctt gca aaa ttg gag ttc aat ata ttt aac tcc tta caa 1022
118 Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln
119 305 310 315
121 caa aag gaa tta caa tat ctt ttg aga tgg tgg aaa gag tcg gat ttg 1070
122 Gln Lys Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu
123 320 325 330
125 cct aaa ttg aca ttt gct cgg cat cgt cat gtg gaa ttc tac act ttg 1118
126 Pro Lys Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu
127 335 340 345 350
129 gcc tct tgt att gcc att gac cca aaa cat tct gca ttc aga cta ggc 1166
130 Ala Ser Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly
131 355 360 365
133 ttc gcc aaa atg tgt cat ctt gtc aca gtt ttg gac gat att tac gac 1214

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DATE: 01/15/2002

TIME: 18:55:54

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Output Set: N:\CRF3\01152002\J025145.raw

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138	Thr	Phe	Gly	Thr	Ile	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ser	Ala	Ile	Lys	
139			385					390					395				
141	aga	tgg	aat	tca	tca	gag	ata	gaa	cac	ctt	cca	gaa	tat	atg	aaa	tgt	1310
142	Arg	Trp	Asn	Ser	Ser	Glu	Ile	Glu	His	Leu	Pro	Glu	Tyr	Met	Lys	Cys	
143		400					405					410					
145	gtg	tac	atg	gtc	gtg	ttt	gaa	act	gta	aat	gaa	ctg	aca	cga	gag	gcg	1358
146	Val	Tyr	Met	Val	Val	Phe	Glu	Thr	Val	Asn	Glu	Leu	Thr	Arg	Glu	Ala	
147	415					420					425					430	
149	gag	aag	act	caa	ggg	aga	aac	act	ctc	aac	tat	gtt	cga	aag	gct	tgg	1406
150	Glu	Lys	Thr	Gln	Gly	Arg	Asn	Thr	Leu	Asn	Tyr	Val	Arg	Lys	Ala	Trp	
151				435					440					445			
153	gag	gct	tat	ttt	gat	tca	tat	atg	gaa	gaa	gca	aaa	tgg	atc	tct	aat	1454
154	Glu	Ala	Tyr	Phe	Asp	Ser	Tyr	Met	Glu	Glu	Ala	Lys	Trp	Ile	Ser	Asn	
155				450					455				460				
157	ggt	tat	ctg	cca	atg	ttt	gaa	gag	tac	cat	gag	aat	ggg	aaa	gtg	agc	1502
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159			465				470					475					
161	tct	gca	tat	cgc	gta	gca	aca	ttg	caa	ccc	atc	ctc	act	ttg	aat	gca	1550
162	Ser	Ala	Tyr	Arg	Val	Ala	Thr	Leu	Gln	Pro	Ile	Leu	Thr	Leu	Asn	Ala	
163		480				485					490						
165	tgg	ctt	cct	gat	tac	atc	ttg	aag	gga	att	gat	ttt	cca	tcc	agg	ttc	1598
166	Trp	Leu	Pro	Asp	Tyr	Ile	Leu	Lys	Gly	Ile	Asp	Phe	Pro	Ser	Arg	Phe	
167	495			500					505						510		
169	aat	gat	ttg	gca	tcg	tcc	ttc	ctt	cgg	cta	cga	ggt	gac	aca	cgc	tgc	1646
170	Asn	Asp	Leu	Ala	Ser	Ser	Phe	Leu	Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	
171				515					520				525				
173	tac	aag	gcc	gat	agg	gat	cgt	ggt	gaa	gaa	gct	tcg	tgt	ata	tca	tgt	1694
174	Tyr	Lys	Ala	Asp	Arg	Asp	Arg	Gly	Glu	Glu	Ala	Ser	Cys	Ile	Ser	Cys	
175			530						535				540				
177	tat	atg	aaa	gac	aat	cct	gga	tca	acc	gaa	gaa	gat	gcc	ctc	aat	cat	1742
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183		560				565					570						
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186	Leu	Arg	Ser	Asn	Asp	Asn	Ile	Pro	Met	Leu	Ala	Lys	Lys	His	Ala	Phe	
187	575			580					585				590				
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190	Asp	Ile	Thr	Arg	Ala	Leu	His	His	Leu	Tyr	Ile	Tyr	Arg	Asp	Gly	Phe	
191				595					600				605				
193	agt	gtt	gcc	aac	aag	gaa	aca	aaa	aaa	ttg	gtt	atg	gaa	aca	ctc	ctt	1934
194	Ser	Val	Ala	Asn	Lys	Glu	Thr	Lys	Lys	Leu	Val	Met	Glu	Thr	Leu	Leu	
195			610						615				620				
197	gaa	tct	atg	ctt	ttt	taa	ctataac	cat	atccata	ata	ataag	ctcat					1982
198	Glu	Ser	Met	Leu	Phe												

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/025,145

DATE: 01/15/2002

TIME: 18:55:54

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222 Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser
223 35 40 45
225 Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg
226 50 55 60
228 Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln
229 65 70 75 80
231 Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu
232 85 90 95
234 Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
235 100 105 110
237 Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
238 115 120 125
240 Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
241 130 135 140
243 Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
244 145 150 155 160
246 Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr
247 165 170 175
249 Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro
250 180 185 190
252 Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser
253 195 200 205
255 Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg
256 210 215 220
258 Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
259 225 230 235 240
261 Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val
262 245 250 255
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265 260 265 270
267 Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu
268 275 280 285
270 Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu
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RAW SEQUENCE LISTING
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DATE: 01/15/2002
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280          340          345          350
282 Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala
283          355          360          365
285 Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe
286          370          375          380
288 Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp
289 385          390          395          400
291 Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr
292          405          410          415
294 Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys
295          420          425          430
297 Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala
298          435          440          445
300 Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr
301          450          455          460
303 Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala
304 465          470          475          480
306 Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu
307          485          490          495
309 Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp
310          500          505          510
312 Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys
313          515          520          525
315 Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met
316          530          535          540
318 Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn
319 545          550          555          560
321 Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg
322          565          570          575
324 Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile
325          580          585          590
327 Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val
328          595          600          605
330 Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser
331          610          615          620
333 Met Leu Phe
334 625

```

337 <210> SEQ ID NO: 3

338 <211> LENGTH: 2018

339 <212> TYPE: DNA

340 <213> ORGANISM: Abies grandis

342 <220> FEATURE:

343 <221> NAME/KEY: CDS

344 <222> LOCATION: (6)..(1892)

345 <223> OTHER INFORMATION: Clone AG3.18 encoding pinene synthase

<210> 11

<211> 108

<212> DNA

<213>

Artificial Sequence

<220>

<223>

<400>

11

gatgatgggt ttgatgcgca cggaacccta gatgaattga agctattcac tgaggctgtg 60
 agaagatggg acctctcctt tacagacaac tccccgatt acatgaaa 108

see item 11 on Euro Summary
 sheet

FYI

Use of n or Xaa has been detected in the Sequence Listing.
 In the sequence listing to insure a corresponding
 translation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

10/025,145 2

<210> 25
<211> 8
<212> PRT
<213> : Artificial Sequence
<220>
<223>

Description of Artificial Sequence: conserved

amino acid motif on which the sequence of Primer D

was based, wherein Xaa at position number 3 represents Thr or Ile, Xaa at

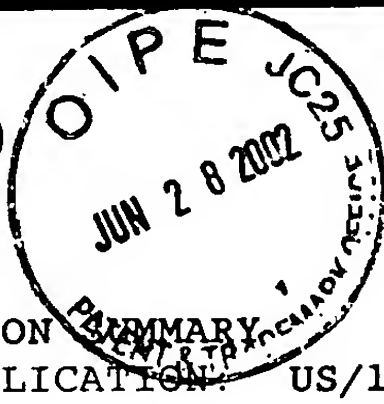
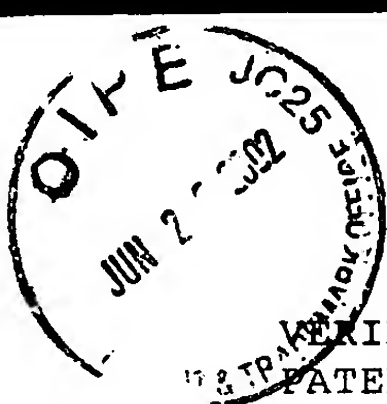
position number 4 represents Ile or Tyr or Phe, Xaa at position number 6

<2207> <223> represents Ala or Val and Xaa at position number 8 represents Ala or Gly

Per 1.823 of Sequence Rules, 4 lines maximum
for <223> response. Insert another <2207 after
4th line and insert a <223> on 5th line.

IMPORTANT:

The types of errors shown exist throughout
the sequence. Please check subsequent
sequences for similar errors.



VERIFICATION SUMMARY
PATENT APPLICATION: US/10/025,145

DATE: 01/15/2002
TIME: 18:55:55

Input Set : A:\18414seq.txt

Output Set: N:\CRF3\01152002\J025145.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:983 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1003 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1031 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1031 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1077 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1949 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1969 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2027 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:2058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:2072 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2081 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:2102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:2609 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:45
L:2609 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:45
L:2609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:2623 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2626 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:2626 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:2626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:2672 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2689 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2692 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:50
L:2692 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:50
L:2692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:2706 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2709 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:51
L:2709 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:2709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:2723 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2726 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:52
L:2726 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:52
L:2726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:2740 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2743 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:53
L:2743 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:53
L:2743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:2786 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:56
L:2786 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:56
L:2786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56